

IN THE SPECIFICATION:

Kindly replace the following paragraphs 0031, 0034-0069, 0071, 0282, and 0294 with the following amended paragraphs:

[0031] Figure 6 shows another comparison of the “most parsimonious reconstruction” methodology and the “maximum likelihood reconstruction methodology” (SEQ ID NOS: 7-23).

[0034] Figure 9 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *gag* gene (SEQ ID NOS: 24-26).

[0035] Figure 10 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *env* (encoding gp160) (SEQ ID NOS: 27 and 28).

[0036] Figure 11 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *nef* gene (SEQ ID NOS: 29-31).

[0037] Figure 12 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *pol* gene (SEQ ID NOS: 32-34).

[0038] Figure 13 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *rev* gene (SEQ ID NOS: 35-37).

[0039] Figure 14 shows a comparison of the Most Recent Common Ancestor (“MRCA”), COT Least Squares (“LScot”) and COT Minimum of Means (“MMcot”) reconstructions for the Clade B *tat* gene (SEQ ID NOS: 38-40).

[0040] Figure 15 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B *vif* gene (SEQ ID NOS: 41 and 42).

[0041] Figure 16 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B *vpr* gene (SEQ ID NOS: 43-44).

[0042] Figure 17 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B *vpu* gene (SEQ ID NOS: 45-46).

[0043] Figure 18 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B gag protein (SEQ ID NOS: 47-49).

[0044] Figure 19 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B gp160 protein (SEQ ID NOS: 50-51).

[0045] Figure 20 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B nef protein (SEQ ID NOS: 52-54).

[0046] Figure 21 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B pol protein (SEQ ID NOS: 55-57).

[0047] Figure 22 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B rev protein (SEQ ID NOS: 58-60).

[0048] Figure 23 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B tat protein (SEQ ID NOS: 61-62).

[0049] Figure 24 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B vif protein (SEQ ID NOS: 63-64).

[0050] Figure 25 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B vpr protein (SEQ ID NOS: 65-67).

[0051] Figure 26 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade B vpu protein (SEQ ID NOS: 68-69).

[0052] Figure 27 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C gag gene (SEQ ID NOS: 70-72).

[0053] Figure 28 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C env (encoding gp160) (SEQ ID NOS: 73-75).

[0054] Figure 29 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C nef gene (SEQ ID NOS: 76-77).

[0055] Figure 30 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C pol gene (SEQ ID NOS: 78-80).

[0056] Figure 31 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C rev* gene (SEQ ID NOS: 81-83).

[0057] Figure 32 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C tat* gene (SEQ ID NOS: 84-86).

[0058] Figure 33 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C vif* gene (SEQ ID NOS: 87-89).

[0059] Figure 34 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C vpr* gene (SEQ ID NOS: 90-92).

[0060] Figure 35 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C vpu* gene (SEQ ID NOS: 93-95).

[0061] Figure 36 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C gag* protein (SEQ ID NOS: 96-98).

[0062] Figure 37 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C gp160* protein (SEQ ID NOS: 99-101).

[0063] Figure 38 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade *C nef* protein (SEQ ID NOS: 102-103).

[0064] Figure 39 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C pol protein (SEQ ID NOS: 104-106).

[0065] Figure 40 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C rev protein (SEQ ID NOS: 107-109).

[0066] Figure 41 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C tat protein (SEQ ID NOS: 110-111).

[0067] Figure 42 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C vif protein (SEQ ID NOS: 112-114).

[0068] Figure 43 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C vpr protein (SEQ ID NOS: 115-117).

[0069] Figure 44 shows a comparison of the Most Recent Common Ancestor ("MRCA"), COT Least Squares ("LScot") and COT Minimum of Means ("MMcot") reconstructions for the Clade C vpu protein (SEQ ID NOS: 118-119).

[0071] Figure 46. Deduced ancestor protein sequences SIVBK28 ancestor (Env segment) and AN1-EnvB (SEQ ID NOS: 120-121).

[0282] Referring to Figure 6, another example illustrates the differences in these methodologies to determine a most recent common ancestor. In this example, twelve sequences of seven nucleotides are presented. These sequences share the illustrated evolutionary history. A consensus sequence calculated from these sequences is CATACTG (SEQ ID NO: 19). In panel A, the maximum likelihood reconstruction of the determined ancestral node is shown as

GATCCTG (SEQ ID NO: 7). Other determined sequences are presented adjacent the other internal nodes. In panel B, the most parsimonious reconstruction at the same nodes is presented. As shown, the most parsimonious reconstruction predicts the consensus sequence GAWCCTG (SEQ ID NO: 8), where “W” symbolizes that either an A or T is equally possible to be at the third position. Similarly other most parsimonious reconstructions are shown at the various internal nodes. At the seventh internal node, the last nucleotide is indicated with the symbol “V” representing that an A, C or G might be present. Also note in this example, the consensus sequence differs in at least two sites (the 1st and 4th positions) from either the maximum likelihood- or parsimony-determined sequence for the MRCA.

[0294] *Ancestral state reconstruction of the SIVmacBK28 env sequence:* SIVmac sequences obtained from a series of experimental infections of rhesus macaques (Edmonson *et al.*, *J. Virol.* 72:405-14 (1998)) were used to reconstruct an ancestral sequence to compare to the plasmid-derived SIV clone used to inoculate these monkeys. A region of *env* from position 8,265 to 8,827 of the SIVmacBK28 genome was amplified by nested-PCR from uncultured PBMC DNA from the SIV infected macaques. First round primers were UP-3, positions (8,117 to 8,130), AGACTGCAGATGTGAAGAGGTACAC (SEQ ID NO:122) and PEXTM6 (8,977 to 8,953), GGATCTGGTATGCTCATAGCAA (SEQ ID NO:123). Second round primers were PEXTM7 (8,265 to 8,286), GATACTGCAGCAACAGCAACAGCTG (SEQ ID NO:124) and UP-5 (8,827 to 8,810), GCAAAGCTTCTCTGGTTGGCAGTG (SEQ ID NO:125). Amplified products were then cloned and sequenced. The GenBank accession numbers for these sequences are AY169007–AY169163. Methods for SIVmacBK28 ancestor reconstruction were identical to those outlined below. The model of evolution is given in Table 12 and the reconstructed sequence is provided in Figure 46.